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| | | |
|--------------|---|---|
| NEWS 1 | Web Page URLs for STN Seminar Schedule - N. America | |
| NEWS 2 | Dec 17 | The CA Lexicon available in the CAPLUS and CA files |
| NEWS 3 | Feb 06 | Engineering Information Encompass files have new names |
| NEWS 4 | Feb 16 | TOXLINE no longer being updated |
| NEWS 5 | Apr 23 | Search Derwent WPINDEX by chemical structure |
| NEWS 6 | Apr 23 | PRE-1967 REFERENCES NOW SEARCHABLE IN CAPLUS AND CA |
| NEWS 7 | May 07 | DGENE Reload |
| NEWS 8 | Jun 20 | Published patent applications (A1) are now in USPATFULL |
| NEWS 9 | JUL 13 | New SDI alert frequency now available in Derwent's DWPI and DPCI |
| NEWS 10 | Aug 23 | In-process records and more frequent updates now in MEDLINE |
| NEWS 11 | Aug 23 | PAGE IMAGES FOR 1947-1966 RECORDS IN CAPLUS AND CA |
| NEWS 12 | Aug 23 | Adis Newsletters (ADISNEWS) now available on STN |
| NEWS 13 | Sep 17 | IMSworld Pharmaceutical Company Directory name change to PHARMASEARCH |
| NEWS 14 | Oct 09 | Korean abstracts now included in Derwent World Patents Index |
| NEWS 15 | Oct 09 | Number of Derwent World Patents Index updates increased |
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| NEWS 17 | Oct 22 | Over 1 million reactions added to CASREACT |
| NEWS 18 | Oct 22 | DGENE GETSIM has been improved |
| NEWS 19 | Oct 29 | AAASD no longer available |
| NEWS 20 | Nov 19 | New Search Capabilities USPATFULL and USPAT2 |
| NEWS 21 | Nov 19 | TOXCENTER(SM) - new toxicology file now available on STN |
| NEWS 22 | Nov 29 | COPPERLIT now available on STN |
| NEWS 23 | Nov 29 | DWPI revisions to NTIS and US Provisional Numbers |
| NEWS 24 | Nov 30 | Files VETU and VETB to have open access |
| NEWS 25 | Dec 10 | WPINDEX/WPIDS/WPIX New and Revised Manual Codes for 2002 |
| NEWS 26 | Dec 10 | DGENE BLAST Homology Search |
| NEWS 27 | Dec 17 | WELDASEARCH now available on STN |
| NEWS 28 | Dec 17 | STANDARDS now available on STN |
| NEWS 29 | Dec 17 | New fields for DPCI |
| NEWS 30 | Dec 19 | CAS Roles modified |
| NEWS 31 | Dec 19 | 1907-1946 data and page images added to CA and CAplus |
| NEWS EXPRESS | August 15 CURRENT WINDOWS VERSION IS V6.0c,
CURRENT MACINTOSH VERSION IS V6.0 (ENG) AND V6.0J (JP),
AND CURRENT DISCOVER FILE IS DATED 07 AUGUST 2001 | |
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(A) LIBRARY IS NOT A RECOGNIZED COMMAND  
The previous command name entered was not recognized by the system.  
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=> s C(a) elegans(p)genom?(a)libr?  
L1           59 C(A) ELEGANS(P) GENOM?(A) LIBR?  
  
=> s C(a) elegans(p)genom?(a)library(p)pheno?  
L2           11 C(A) ELEGANS(P) GENOM?(A) LIBRARY(P) PHENO?
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=> display total ibib abs L2

L2 ANSWER 1 OF 11 MEDLINE
ACCESSION NUMBER: 1999234093 MEDLINE
DOCUMENT NUMBER: 99234093 PubMed ID: 10216251
TITLE: Identification and characterization of a serine hydroxymethyltransferase isoform in *Caenorhabditis briggsae*.
AUTHOR: Watcher G P; Barbazuk W B; O'Neil N J; Marra M A; Ha T; Baillie D L
CORPORATE SOURCE: Institute of Molecular Biology and Biochemistry, Simon Fraser University, Burnaby, British Columbia, Canada.
SOURCE: GENE, (1999 Apr 16) 230 (2) 137-44.
PUB. COUNTRY: Journal code: FOP; 7706761. ISSN: 0378-1119.
Netherlands
LANGUAGE: Journal; Article; (JOURNAL ARTICLE)
English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199906
ENTRY DATE: Entered STN: 19990614
Last Updated on STN: 19990614

Entered Medline: 19990601

AB In the nematode *Caenorhabditis elegans*, the maternal effect lethal gene *mel-32* encodes a serine hydroxymethyltransferase isoform. Since interspecies DNA comparison is a valuable tool for identifying sequences that have been conserved because of their functional importance or role in regulating gene activity, *mel-32*(SHMT) genomic DNA from *C. elegans* was used to screen a **genomic library** from the closely related nematode *Caenorhabditis briggsae*. The *C. briggsae* genomic clone identified fully rescues the *Mel-32* **phenotype** in *C. elegans*, indicating functional and regulatory conservation. Computer analysis reveals that CbMEL-32(SHMT) is 92% identical (97% similar) to CeMEL-32(SHMT) at the amino acid level over the entire length of the protein (484 amino acids), whereas the coding DNA is 82.5% identical (over 1455 nucleotides). Several highly conserved non-coding regions upstream and downstream of the *mel-32*(SHMT) gene reveal potential regulatory sites that may bind trans-acting protein factors.

L2 ANSWER 2 OF 11 MEDLINE

ACCESSION NUMBER: 96234073 MEDLINE

DOCUMENT NUMBER: 96234073 PubMed ID: 8650202

TITLE: Molecular cloning of the Golgi apparatus uridine diphosphate-N-acetylglucosamine transporter from *Kluyveromyces lactis*.

AUTHOR: Abeijon C; Robbins P W; Hirschberg C B

CORPORATE SOURCE: Department of Biochemistry and Molecular Biology,
University of Massachusetts Medical Center, Worcester,
01655, USA.

CONTRACT NUMBER: GM 30365 (NIGMS)
GM 45188 (NIGMS)

SOURCE: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE
UNITED STATES OF AMERICA, (1996 Jun 11) 93 (12) 5963-8.
Journal code: PV3; 7505876. ISSN: 0027-8424.

PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-U48413

ENTRY MONTH: 199607

ENTRY DATE: Entered STN: 19960805

Last Updated on STN: 19960805
Entered Medline: 19960725

AB The mannan chains of *Kluyveromyces lactis* mannoproteins are similar to those of *Saccharomyces cerevisiae* except that they lack mannose phosphate and have terminal alpha1-->2-linked N-acetylglucosamine. The biosynthesis of these chains probably occurs in the lumen of the Golgi apparatus, by analogy to *S. cerevisiae*. The sugar donors, GDP-mannose and UDP-GlcNAc, must first be transported from the cytosol, their site of synthesis, via specific Golgi membrane transporters into the lumen where they are substrates in the biosynthesis of these mannoproteins. A mutant of *K. lactis*, mnn2-2, that lacks terminal N-acetylglucosamine in its mannan chains in vivo, has recently been characterized and shown to have a specific defect in transport of UDP-GlcNAc into the lumen of Golgi vesicles in vitro. We have now cloned the gene encoding the *K. lactis* Golgi membrane UDP-GlcNAc transporter by complementation of the mnn2-2 mutation. The mnn2-2 mutant was transformed with a **genomic library** from wild-type *K. lactis* in a pKD1-derived vector; transformants were isolated and **phenotypic** correction was monitored following cell surface labeling with fluorescein isothiocyanate conjugated to *Griffonia simplicifolia* II lectin, which binds terminal N-acetylglucosamine, and a fluorescent activated cell sorter. A 2.4-kb DNA fragment was found to restore the wild-type lectin binding **phenotype**. Upon loss of the plasmid containing this fragment, reversion to the mutant **phenotype** occurred. The above fragment contained an open reading frame for a multitransmembrane spanning protein

of 328 amino acids. The protein contains a leucine zipper motif and has high homology to predicted proteins from *S. cerevisiae* and *C. elegans*. In an assay in vitro, Golgi vesicles isolated from the transformant had regained their ability to transport UDP-GlcNAc. Taken together, the above results strongly suggest that the cloned gene encodes the Golgi UDP-GlcNAc transporter of *K. lactis*.

L2 ANSWER 3 OF 11 BIOSIS COPYRIGHT 2002 BIOSIS
ACCESSION NUMBER: 1999:248195 BIOSIS
DOCUMENT NUMBER: PREV199900248195
TITLE: Identification and characterization of a serine hydroxymethyltransferase isoform in *Caenorhabditis briggsae*.
AUTHOR(S): Vatcher, G. P.; Barbazuk, W. B.; O'Neil, N. J.; Marra, M. A.; Ha, T.; Baillie, D. L. (1)
CORPORATE SOURCE: (1) Institute of Molecular Biology and Biochemistry, Simon Fraser University, Burnaby, British Columbia, V5A 1S6 Canada
SOURCE: Gene (Amsterdam), (April 16, 1999) Vol. 230, No. 2, pp. 137-144.
ISSN: 0378-1119.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English

AB In the nematode *Caenorhabditis elegans*, the maternal effect lethal gene *mel-32* encodes a serine hydroxymethyltransferase isoform. Since interspecies DNA comparison is a valuable tool for identifying sequences that have been conserved because of their functional importance or role in regulating gene activity, *mel-32*(SHMT) genomic DNA from *C. elegans* was used to screen a **genomic library** from the closely related nematode *Caenorhabditis briggsae*. The *C. briggsae* genomic clone identified fully rescues the *Mel-32* **phenotype** in *C. elegans*, indicating functional and regulatory conservation. Computer analysis reveals that CbMEL-32(SHMT) is 92% identical (97% similar) to CeMEL-32(SHMT) at the amino acid level over the entire length of the protein (484 amino acids), whereas the coding DNA is 82.5% identical (over 1455 nucleotides). Several highly conserved non-coding regions upstream and downstream of the *mel-32*(SHMT) gene reveal potential regulatory sites that may bind trans-acting protein factors.

L2 ANSWER 4 OF 11 BIOSIS COPYRIGHT 2002 BIOSIS
ACCESSION NUMBER: 1996:332779 BIOSIS
DOCUMENT NUMBER: PREV199699055135
TITLE: Molecular cloning of the Golgi apparatus uridine diphosphate-N-acetylglucosamine transporter from *Kluyveromyces lactis*.
AUTHOR(S): Abeijon, Claudia (1); Robbins, Phillips W.; Hirschberg, Carlos B. (1)
CORPORATE SOURCE: (1) Dep. Biochem.. Mol. Biol., Univ. Mass. Med. Cent., Worcester, MA 01655 USA
SOURCE: Proceedings of the National Academy of Sciences of the United States of America, (1996) Vol. 93, No. 12, pp. 5963-5968.
ISSN: 0027-8424.
DOCUMENT TYPE: Article
LANGUAGE: English

AB The mannan chains of *Kluyveromyces lactis* mannoproteins are similar to those of *Saccharomyces cerevisiae* except that they lack mannose phosphate and have terminal alpha-1 foward 2-linked N-acetylglucosamine. The biosynthesis of these chains probably occurs in the lumen of the Golgi apparatus, by analogy to *S. cerevisiae*. The sugar donors, GDP-mannose and UDP-GlcNAc, must first be transported from the cytosol, their site of synthesis, via specific Golgi membrane transporters into the lumen where they are substrates in the biosynthesis of these mannoproteins. A mutant

of *K. lactis*, mnn2-2, that lacks terminal N-acetylglucosamine in its mannan chains in vivo, has recently been characterized and shown to have a specific defect in transport of UDP-GlcNAc into the lumen of Golgi vesicles in vitro. We have now cloned the gene encoding the *K. lactis* Golgi membrane UDP-GlcNAc transporter by complementation of the mnn2-2 mutation. The mnn2-2 mutant was transformed with a genomic library from wild-type *K. lactis* in a pKD1-derived vector; transformants were isolated and phenotypic correction was monitored following cell surface labeling with fluorescein isothiocyanate conjugated to Griffonia simplicifolia II lectin, which binds terminal N-acetylglucosamine, and a fluorescent activated cell sorter. A 2.4-kb DNA fragment was found to restore the wild-type lectin binding phenotype. Upon loss of the plasmid containing this fragment, reversion to the mutant phenotype occurred. The above fragment contained an open reading frame for a multitransmembrane spanning protein of 328 amino acids. The protein contains a leucine zipper motif and has high homology to predicted proteins from *S. cerevisiae* and *C. elegans*. In an assay in vitro, Golgi vesicles isolated from the transformant had regained their ability to transport UDP-GlcNAc. Taken together, the above results strongly suggest that the cloned gene encodes the Golgi UDP-GlcNAc transporter of *K. lactis*.

L2 ANSWER 5 OF 11 CAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 2000:35000 CAPLUS

DOCUMENT NUMBER: 132:103727

TITLE: Characterization of gene function using double-stranded RNA inhibition

INVENTOR(S): Plaetinck, Geert; Platteeuw, Christ; Mortier, Katherine; Bogaert, Thierry

PATENT ASSIGNEE(S): Devgen N.V., Belg.

SOURCE: PCT Int. Appl., 97 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|---|------|----------|-----------------|-------------|
| WO 2000001846 | A2 | 20000113 | WO 1999-EP4718 | 19990702 |
| WO 2000001846 | A3 | 20000615 | | |
| W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM | | | | |
| RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG | | | | |
| AU 9949079 | A1 | 20000124 | AU 1999-49079 | 19990702 |
| GB 2349885 | A1 | 20001115 | GB 2000-20485 | 19990702 |
| EP 1093526 | A2 | 20010425 | EP 1999-932836 | 19990702 |
| R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO | | | | |
| GB 2362885 | A1 | 20011205 | GB 2001-18514 | 19990702 |
| NO 2001000019 | A | 20010305 | NO 2001-19 | 20010102 |
| PRIORITY APPLN. INFO.: | | | GB 1998-14536 | A 19980703 |
| | | | GB 1998-27152 | A 19981209 |
| | | | GB 2000-20485 | A3 19990702 |
| | | | WO 1999-EP4718 | W 19990702 |

AB There is provided a method of identifying DNA responsible for conferring a particular phenotype in a cell which method comprises (a) constructing a cDNA or genomic library of the DNA of

said cell in a suitable vector in an orientation relative to a promoter(s) capable of initiating transcription of said cDNA or DNA to double-stranded (ds) RNA upon binding of an appropriate transcription factor to said promoter(s), (b) introducing said library into one or more of said cells comprising said transcription factor, and (c) identifying and isolating a particular **phenotype** of said cell comprising said library and identifying the DNA or cDNA fragment from said library responsible for conferring said **phenotype**. Using this technique it is also possible to assign function to a known DNA sequence by (a) identifying a homolog(s) of said DNA sequence in a cell, (b) isolating the relevant DNA homolog(s) or a fragment thereof from said cell, (c) cloning said homolog or fragment thereof into an appropriate vector in an orientation relative to a suitable promoter(s) capable of initiating transcription of dsRNA from said DNA homolog or fragment upon binding of an appropriate transcription factor to said promoter(s), and (d) introducing said vector into said cell from step (a) comprising said transcription factor. Thus, an ordered library for inhibitory dsRNA technol. can be prep'd. harboring every gene of the *Caenorhabditis elegans* genome; the resulting **phenotypes** can give a functional description to the gene or gene family or gene homologs of the *C. elegans* genome. Plasmid vectors are described incorporating phage T3, T7, and SP6 RNA polymerase genes and promoters for expression in *C. elegans*. Inhibitory dsRNA technol. can also be used to validate clones identified in yeast 2-hybrid vector expts.

L2 ANSWER 6 OF 11 CAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 1999:300425 CAPLUS

DOCUMENT NUMBER: 131:126184

TITLE: Identification and characterization of a serine hydroxymethyltransferase isoform in *Caenorhabditis briggsae*

AUTHOR(S): Vatcher, G. P.; Barbazuk, W. B.; O'Neil, N. J.; Marra, M. A.; Ha, T.; Baillie, D. L.

CORPORATE SOURCE: Institute of Molecular Biology and Biochemistry, Simon Fraser University, Burnaby, BC, V5A 1S6, Can.

SOURCE: Gene (1999), 230(2), 137-144

CODEN: GENED6; ISSN: 0378-1119

PUBLISHER: Elsevier Science B.V.

DOCUMENT TYPE: Journal

LANGUAGE: English

AB In the nematode *Caenorhabditis elegans*, the maternal effect lethal gene *mel-32* encodes a serine hydroxymethyltransferase isoform. Since interspecies DNA comparison is a valuable tool for identifying sequences that have been conserved because of their functional importance or role in regulating gene activity, *mel-32*(SHMT) genomic DNA from *C. elegans* was used to screen a **genomic library** from the closely related nematode *Caenorhabditis briggsae*. The *C. briggsae* genomic clone identified fully rescues the *Mel-32 phenotype* in *C. elegans*, indicating functional and regulatory conservation. Computer anal. reveals that CbMEL-32(SHMT) is 92% identical (97% similar) to CeMEL-32(SHMT) at the amino acid level over the entire length of the protein (484 amino acids), whereas the coding DNA is 82.5% identical (over 1455 nucleotides). Several highly conserved noncoding regions upstream and downstream of the *mel-32*(SHMT) gene reveal potential regulatory sites that may bind trans-acting protein factors.

REFERENCE COUNT: 38

- REFERENCE(S):
- (1) Altschul, S; J Mol Biol 1990, V215, P403 CAPLUS
 - (3) de Bono, M; Genetics 1996, V144, P587 CAPLUS
 - (4) Emmons, S; Proc Natl Acad Sci USA 1979, V76, P1333 CAPLUS
 - (5) Garrow, T; J Biol Chem 1993, V268, P11910 CAPLUS
 - (6) Gilleard, J; Gene 1997, V193, P181 CAPLUS
- ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 7 OF 11 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1996:367026 CAPLUS
DOCUMENT NUMBER: 125:50470
TITLE: Molecular cloning of the Golgi apparatus uridine diphosphate-N-acetylglucosamine transporter from *Kluyveromyces lactis*
AUTHOR(S): Abeijon, Claudia; Robbins, Phillips W.; Hirschberg, Carlos B.
CORPORATE SOURCE: Dep. Biochem. Mol. Biol., Univ. Massachusetts Med. Cent., Worcester, MA, 01655, USA
SOURCE: Proc. Natl. Acad. Sci. U. S. A. (1996), 93(12), 5963-5968
CODEN: PNASA6; ISSN: 0027-8424
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The mannan chains of *Kluyveromyces lactis* mannoproteins are similar to those of *Saccharomyces cerevisiae* except that they lack mannose phosphate and have terminal .alpha.1.fwdarw.2-linked N-acetylglucosamine. The biosynthesis of these chains probably occurs in the human of the Golgi app., by analogy to *S. cerevisiae*. The sugar donors, GDP-mannose and UDP-GlcNAc, must first be transported from the cytosol, their site of synthesis, via specific Golgi membrane transporters into the lumen where they are substrates in the biosynthesis of these mannoproteins. A mutant of *K. lactis*, mnn2-2, that lacks terminal N-acetylglucosamine in its mannan chains in vivo, has recently been characterized and shown to have a specific defect in transport of UDP-GlcNAc into the lumen of Golgi vesicles in vitro. We have now cloned the gene encoding the *K. lactis* Golgi membrane UDP-GlcNAc transporter by complementation of the mnn2-2 mutation. The mnn2-2 mutant was transformed with a **genomic library** from wild-type *K. lactis* in a pKD1-derived vector; transformants were isolated and **phenotypic** correction was monitored following cell surface labeling with fluorescein isothiocyanate conjugated to *Griffonia simplicifolia* II lectin, which binds terminal N-acetylglucosamine, and a fluorescent activated cell sorter. A 2.4-kb DNA fragment was found to restore the wild-type lectin binding **phenotype**. Upon loss of the plasmid contg. this fragment, reversion to the mutant **phenotype** occurred. The above fragment contained an open reading frame for a multitransmembrane spanning protein of 328 amino acids. The protein contains a leucine zipper motif and has high homol. to predicted proteins from *S. cerevisiae* and *C. elegans*. In an assay in vitro, Golgi vesicles isolated from the transformant had regained their ability to transport UDP-GlcNAc. Taken together, the above results strongly suggest that the cloned gene encodes the golgi UDP-GlcNAc transporter of *K. lactis*.

L2 ANSWER 8 OF 11 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
ACCESSION NUMBER: 1999149080 EMBASE
TITLE: Identification and characterization of a serine hydroxymethyltransferase isoform in *Caenorhabditis briggsae*.
AUTHOR: Vatcher G.P.; Barbazuk W.B.; O'Neil N.J.; Marra M.A.; Ha T.; Baillie D.L.
CORPORATE SOURCE: D.L. Baillie, Inst. of Molec. Biology/Biochemistry, Simon Fraser University, Burnaby, BC V5A 1S6, Canada
SOURCE: Gene, (16 Apr 1999) 230/2 (137-144).
Refs: 38
ISSN: 0378-1119 CODEN: GENED6
PUBLISHER IDENT.: S 0378-1119(99)00076-1
COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 004 Microbiology
LANGUAGE: English
SUMMARY LANGUAGE: English

AB In the nematode *Caenorhabditis elegans*, the maternal effect lethal gene *mel-32* encodes a serine hydroxymethyltransferase isoform. Since interspecies DNA comparison is a valuable tool for identifying sequences that have been conserved because of their functional importance or role in regulating gene activity, *mel-32*(SHMT) genomic DNA from *C. elegans* was used to screen a **genomic library** from the closely related nematode *Caenorhabditis briggsae*. The *C. briggsae* genomic clone identified fully rescues the *Mel-32 phenotype* in *C. elegans*, indicating functional and regulatory conservation. Computer analysis reveals that *CbMEL-32*(SHMT) is 92% identical (97% similar) to *CeMEL-32*(SHMT) at the amino acid level over the entire length of the protein (484 amino acids), whereas the coding DNA is 82.5% identical (over 1455 nucleotides). Several highly conserved non-coding regions upstream and downstream of the *mel-32*(SHMT) gene reveal potential regulatory sites that may bind trans-acting protein factors.

L2 ANSWER 9 OF 11 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.

ACCESSION NUMBER: 96188142 EMBASE

DOCUMENT NUMBER: 1996188142

TITLE: Molecular cloning of the Golgi apparatus uridine diphosphate-N-acetylglucosamine transporter from *Kluyveromyces lactis*.

AUTHOR: Abeijon C.; Robbins P.W.; Hirschberg C.B.

CORPORATE SOURCE: Biochemistry/Molecular Biology Dept., Massachusetts Univ. Medical Center, Worcester, MA 01655, United States

SOURCE: Proceedings of the National Academy of Sciences of the United States of America, (1996) 93/12 (5963-5968).

ISSN: 0027-8424 CODEN: PNASA6

COUNTRY: United States

DOCUMENT TYPE: Journal; Article

FILE SEGMENT: 004 Microbiology

LANGUAGE: English

SUMMARY LANGUAGE: English

AB The mannan chains of *Klyveromyces lactis* mannoproteins are similar to those of *Saccharomyces cerevisiae* except that they lack mannose phosphate and have terminal α .1.fwdarw.2-linked N-acetylglucosamine. The biosynthesis of these chains probably occurs in the lumen of the Golgi apparatus, by analogy to *S. cerevisiae*. The sugar donors, GDP-mannose and UDP-GlcNAc, must first be transported from the cytosol, their site of synthesis, via specific Golgi membrane transporters into the lumen where they are substrates in the biosynthesis of these mannoproteins. A mutant of *K. lactis*, *mnn2-2*, that lacks terminal N-acetylglucosamine in its mannan chains *in vivo*, has recently been characterized and shown to have a specific defect in transport of UDP-GlcNAc into the lumen of Golgi vesicles *in vitro*. We have now cloned the gene encoding the *K. lactis* Golgi membrane UDP-GlcNAc transporter by complementation of the *mnn2-2* mutation. The *mnn2-2* mutant was transformed with a **genomic library** from wild-type *K. lactis* in a pKD1-derived vector; transformants were isolated and **phenotypic** correction was monitored following cell surface labeling with fluorescein isothiocyanate conjugated to *Griffonia simplicifolia* II lectin, which binds terminal N-acetylglucosamine, and a fluorescent activated cell sorter. A 2.4-kb DNA fragment was found to restore the wild-type lectin binding **phenotype**. Upon loss of the plasmid containing this fragment, reversion to the mutant **phenotype** occurred. The above fragment contained an open reading frame for a multitransmembrane spanning protein of 328 amino acids. The protein contains a leucine zipper motif and has high homology to predicted proteins from *S. cerevisiae* and *C. elegans*. In an assay *in vitro*, Golgi vesicles isolated from the transformant had regained their ability to transport UDP-GlcNAc. Taken together, the above results strongly suggest that the cloned gene encodes the Golgi UDP-GlcNAc transporter of *K. lactis*.

L2 ANSWER 10 OF 11 SCISEARCH COPYRIGHT 2002 ISI (R)

ACCESSION NUMBER: 1999:343249 SCISEARCH
THE GENUINE ARTICLE: 190LA
TITLE: Identification and characterization of a serine hydroxymethyltransferase isoform in *Caenorhabditis briggsae*
AUTHOR: Vatcher G P; Barbazuk W B; ONeil N J; Marra M A; Ha T; Baillie D L (Reprint)
CORPORATE SOURCE: SIMON FRASER UNIV, INST MOL BIOL & BIOCHEM, BURNABY, BC V5A 1S6, CANADA (Reprint); SIMON FRASER UNIV, INST MOL BIOL & BIOCHEM, BURNABY, BC V5A 1S6, CANADA; WASHINGTON UNIV, SCH MED, GENOME SEQUENCING CTR, ST LOUIS, MO 63108
COUNTRY OF AUTHOR: CANADA; USA
SOURCE: GENE, (16 APR 1999) Vol. 230, No. 2, pp. 137-144.
Publisher: ELSEVIER SCIENCE BV, PO BOX 211, 1000 AE AMSTERDAM, NETHERLANDS.
ISSN: 0378-1119.

DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: English
REFERENCE COUNT: 38

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB In the nematode *Caenorhabditis elegans*, the maternal effect lethal gene *mel-32* encodes a serine hydroxymethyltransferase isoform. Since interspecies DNA comparison is a valuable tool for identifying sequences that have been conserved because of their functional importance or role in regulating gene activity, *mel-32*(SHMT) genomic DNA from *C. elegans* was used to screen a genomic library from the closely related nematode *Caenorhabditis briggsae*. The *C. briggsae* genomic clone identified fully rescues the *Mel-32* phenotype in *C. elegans*, indicating functional and regulatory conservation. Computer analysis reveals that *CbMEL-32*(SHMT) is 92% identical (97% similar) to *CeMEL-32*(SHMT) at the amino acid level over the entire length of the protein (484 amino acids), whereas the coding DNA is 82.5% identical (over 1455 nucleotides). Several highly conserved noncoding regions upstream and downstream of the *mel-32*(SHMT) gene reveal potential regulatory sites that may bind trans-acting protein factors, (C) 1999 Published by Elsevier Science B.V. All rights reserved.

L2 ANSWER 11 OF 11 SCISEARCH COPYRIGHT 2002 ISI (R)

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TITLE: MOLECULAR-CLONING OF THE GOLGI-APPARATUS URIDINE DIPHOSPHATE-N-ACETYLGLUCOSAMINE TRANSPORTER FROM *KLUYVEROMYCES-LACTIS*
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AB The mannan chains of *Klyveromyces lactis* mannoproteins are similar to those of *Saccharomyces cerevisiae* except that they lack mannose phosphate and have terminal alpha 1-->2-linked N-acetylglucosamine. The biosynthesis of these chains probably occurs in the lumen of the Golgi apparatus, by analogy to *S. cerevisiae*. The sugar donors, GDP-mannose and UDP-GlcNAc, must first be transported from the cytosol, their site of synthesis, via

specific Golgi membrane transporters into the lumen where they are substrates in the biosynthesis of these mannoproteins. A mutant of *K. lactis*, mnn2-2, that lacks terminal N-acetylglucosamine in its mannan chains in vivo, has recently been characterized and shown to have a specific defect in transport of UDP-GlcNAc into the lumen of Golgi vesicles in vitro. We have now cloned the gene encoding the *K. lactis* Golgi membrane UDP-GlcNAc transporter by complementation of the mnn2-2 mutation. The mnn2-2 mutant was transformed with a **genomic library** from wild-type *K. lactis* in a pKD1-derived vector; transformants were isolated and **phenotypic** correction was monitored following cell surface labeling with fluorescein isothiocyanate conjugated to *Griffonia simplicifolia* II lectin, which binds terminal N-acetylglucosamine, and a fluorescent activated cell sorter. A 2.4-kb DNA fragment was found to restore the wild-type lectin binding **phenotype**. Upon loss of the plasmid containing this fragment, reversion to the mutant **phenotype** occurred. The above fragment contained an open reading frame for a multitransmembrane spanning protein of 328 amino acids. The protein contains a leucine zipper motif and has high homology to predicted proteins from *S. cerevisiae* and *C. elegans*. In an assay in vitro, Golgi vesicles isolated from the transformant had regained their ability to transport UDP-GlcNAc. Taken together, the above results strongly suggest that the cloned gene encodes the Golgi UDP-GlcNAc trans porter of *K. lactis*.